



1652

RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/09/441,055A

TIME: 13:18:42

Input Set : A:\001010570.txt

Output Set: N:\CRF3\02282002\I441055A.raw

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3 <110> APPLICANT: USUDA, YOSHIHIRO
4   KURAHASHI, OSAMU
6 <120> TITLE OF INVENTION: METHOD FOR PRODUCING L-METHIONINE BY FERMENTATION
8 <130> FILE REFERENCE: 0010-1057-0
10 <140> CURRENT APPLICATION NUMBER: 09/441,055A
11 <141> CURRENT FILING DATE: 1999-11-16
13 <150> PRIOR APPLICATION NUMBER: JP 10-326717
14 <151> PRIOR FILING DATE: 1998-11-17
16 <160> NUMBER OF SEQ ID NOS: 29
18 <170> SOFTWARE: PatentIn version 3.1
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23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Synthetic DNA
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127 cacagacgca tgccc                                75
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141 aaattttaag ctccc                                75

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158 <212> TYPE: DNA
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219 <213> ORGANISM: Escherichia coli
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222 <221> NAME/KEY: CDS
223 <222> LOCATION: (1)..(1152)
224 <223> OTHER INFORMATION:
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229 Met Ala Lys His Leu Phe Thr Ser Glu Ser Val Ser Glu Gly His Pro
230 1 5 10 15
232 gac aaa att gct gac caa att tct gat gcc gtt tta gac gcg atc ctc      96
233 Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu
234 20 25 30
236 gaa cag gat ccg aaa gca cgc gtt gct tgc gaa acc tac gta aaa acc      144
237 Glu Gln Asp Pro Lys Ala Arg Val Ala Cys Glu Thr Tyr Val Lys Thr
238 35 40 45
240 ggc atg gtt tta gtt ggc ggc gaa atc acc acc agc gcc tgg gta gac      192
241 Gly Met Val Leu Val Gly Gly Glu Ile Thr Thr Ser Ala Trp Val Asp
242 50 55 60
244 atc gaa gag atc acc cgt aac acc gtt cgc gaa att ggc tat gtg cat      240
245 Ile Glu Glu Ile Thr Arg Asn Thr Val Arg Glu Ile Gly Tyr Val His
246 65 70 75 80
248 tcc gac atg ggc ttt gac gct aac tcc tgt gcg gtt ctg agc gct atc      288
249 Ser Asp Met Gly Phe Asp Ala Asn Ser Cys Ala Val Leu Ser Ala Ile
250 85 90 95
252 ggc aaa cag tct cct gac atc aac cag ggc gtt gac cgt gcc gat ccg      336
253 Gly Lys Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Ala Asp Pro
254 100 105 110
256 ctg gaa cag ggc gcg ggt gac cag ggt ctg atg ttt ggc tac gca act      384
257 Leu Glu Gln Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr
258 115 120 125
260 aat gaa acc gac gtg ctg atg cca gca cct atc acc tat gca cac cgt      432
261 Asn Glu Thr Asp Val Leu Met Pro Ala Pro Ile Thr Tyr Ala His Arg
262 130 135 140
264 ctg gta cag cgt cag gct gaa gtg cgt aaa aac ggc act ctg ccg tgg      480
265 Leu Val Gln Arg Gln Ala Glu Val Arg Lys Asn Gly Thr Leu Pro Trp
266 145 150 155 160
268 ctg cgc ccg gac gcg aaa agc cag gtg act ttt cag tat gac gac ggc      528
269 Leu Arg Pro Asp Ala Lys Ser Gln Val Thr Phe Gln Tyr Asp Asp Gly
270 165 170 175
272 aaa atc gtt ggt atc gat gct gtc gtg ctt tcc act cag cac tct gaa      576
273 Lys Ile Val Gly Ile Asp Ala Val Val Leu Ser Thr Gln His Ser Glu
274 180 185 190
276 gag atc gac cag aaa tcg ctg caa gaa gcg gta atg gaa gag atc atc      624
277 Glu Ile Asp Gln Lys Ser Leu Gln Glu Ala Val Met Glu Glu Ile Ile
278 195 200 205
280 aag cca att ctg ccc gct gaa tgg ctg act tct gcc acc aaa ttc ttc      672
281 Lys Pro Ile Leu Pro Ala Glu Trp Leu Thr Ser Ala Thr Lys Phe Phe

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282      210      215      220
284 atc aac ccg acc ggt cgt ttc gtt atc ggt ggc cca atg ggt gac tgc      720
285 Ile Asn Pro Thr Gly Arg Phe Val Ile Gly Gly Pro Met Gly Asp Cys
286 225      230      235      240
288 ggt ctg act ggt cgt aaa att atc gtt gat acc tac ggc ggc atg gcg      768
289 Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala
290      245      250      255
292 cgt cac ggt ggc ggt gca ttc tct ggt aaa gat cca tca aaa gtg gac      816
293 Arg His Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp
294      260      265      270
296 cgt tcc gca gcc tac gca gca cgt tat gtc gcg aaa aac atc gtt gct      864
297 Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Ile Val Ala
298      275      280      285
300 gct ggc ctg gcc gat cgt tgt gaa att cag gtt tcc tac gca atc ggc      912
301 Ala Gly Leu Ala Asp Arg Cys Glu Ile Gln Val Ser Tyr Ala Ile Gly
302      290      295      300
304 gtg gct gaa ccg acc tcc atc atg gta gaa act ttc ggt act gag aaa      960
305 Val Ala Glu Pro Thr Ser Ile Met Val Glu Thr Phe Gly Thr Glu Lys
306 305      310      315      320
308 gtg cct tct gaa caa ctg acc ctg ctg gta cgt gag ttc ttc gac ctg      1008
309 Val Pro Ser Glu Gln Leu Thr Leu Leu Val Arg Glu Phe Phe Asp Leu
310      325      330      335
312 cgc cca tac ggt ctg att cag atg ctg gat ctg ctg cac ccg atc tac      1056
313 Arg Pro Tyr Gly Leu Ile Gln Met Leu Asp Leu Leu His Pro Ile Tyr
314      340      345      350
316 aaa gaa acc gca gca tac ggt cac ttt ggt cgt gaa cat ttc ccg tgg      1104
317 Lys Glu Thr Ala Ala Tyr Gly His Phe Gly Arg Glu His Phe Pro Trp
318      355      360      365
320 gaa aaa acc gac aaa gcg cag ctg ctg cgc gat gct gcc ggt ctg aag      1152
321 Glu Lys Thr Asp Lys Ala Gln Leu Leu Arg Asp Ala Ala Gly Leu Lys
322      370      375      380
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328 <211> LENGTH: 384
329 <212> TYPE: PRT
330 <213> ORGANISM: Escherichia coli
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335 1      5      10      15
338 Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu
339      20      25      30
342 Glu Gln Asp Pro Lys Ala Arg Val Ala Cys Glu Thr Tyr Val Lys Thr
343      35      40      45
346 Gly Met Val Leu Val Gly Gly Glu Ile Thr Thr Ser Ala Trp Val Asp
347      50      55      60
350 Ile Glu Glu Ile Thr Arg Asn Thr Val Arg Glu Ile Gly Tyr Val His
351 65      70      75      80
354 Ser Asp Met Gly Phe Asp Ala Asn Ser Cys Ala Val Leu Ser Ala Ile
355      85      90      95

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VERIFICATION SUMMARY

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